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c	691	15.2	0.3	20	1	US-08-983-605-245	Sequence 245, App
c	692	15.2	0.3	20	1	US-09-802-669-177	Sequence 177, App
c	693	15.2	0.3	20	1	US-09-854-883-305	Sequence 305, App
c	694	15.2	0.3	20	1	US-09-817-135B-15	Sequence 15, Appl
c	695	15.2	0.3	20	1	US-09-791-243-31	Sequence 31, Appl
c	696	15.2	0.3	20	1	US-09-734-672-61	Sequence 61, Appl
c	697	15.2	0.3	20	1	US-09-982-828-61	Sequence 61, Appl
c	698	15.2	0.3	20	1	US-09-784-674-549	Sequence 549, App
c	699	15.2	0.3	20	1	US-09-917-963-44	Sequence 44, Appl
c	700	15.2	0.3	20	1	US-09-923-327-125	Sequence 125, App
c	701	15.2	0.3	20	1	US-09-954-679-77	Sequence 77, Appl
c	702	15.2	0.3	20	1	US-10-022-819-56	Sequence 56, Appl
c	703	15.2	0.3	20	1	US-10-238-443-51	Sequence 51, Appl
c	704	15.2	0.3	20	1	US-10-094-458A-15	Sequence 15, Appl
c	705	15.2	0.3	20	1	US-10-452-002A-42	Sequence 42, Appl
c	706	15.2	0.3	20	1	US-10-309-362-51	Sequence 51, Appl
c	707	15.2	0.3	20	1	US-10-174-794-9	Sequence 9, Appli
c	708	15.2	0.3	20	1	US-10-109-349A-4	Sequence 4, Appli
c	709	15.2	0.3	20	1	US-10-021-707-34	Sequence 34, Appl
c	710	15.2	0.3	20	1	US-10-263-655-15	Sequence 15, Appl
c	711	15.2	0.3	20	1	US-10-360-510-305	Sequence 305, App
c	712	15.2	0.3	20	1	US-10-160-497-81	Sequence 81, Appl
c	713	15.2	0.3	20	1	US-10-348-750-81	Sequence 81, Appl
c	714	15.2	0.3	20	1	US-10-348-750-138	Sequence 138, App
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c	717	15.2	0.3	20	1	US-10-452-002A-42	Sequence 42, Appl
c	718	15.2	0.3	20	1	US-10-189-268-39	Sequence 39, Appl
c	719	15.2	0.3	20	1	US-10-189-268-109	Sequence 109, App
c	720	15.2	0.3	20	1	US-10-349-143-4301	Sequence 4301, Ap
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c	724	15.2	0.3	20	1	US-10-199-676-29	Sequence 29, Appl
c	725	15.2	0.3	20	1	US-10-199-676-65	Sequence 65, Appl
c	726	15.2	0.3	20	1	US-10-619-220-177	Sequence 177, App
c	727	15.2	0.3	20	1	US-10-673-063-34	Sequence 34, Appl
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c	781	15.2	0.3	20	1	US-10-697-527-245	Sequence 245, App
c	782	15.2	0.3	20	1	US-11-008-747-305	Sequence 305, App

ALIGNMENTS

RESULT 1
US-09-908-975-10633
Sequence 10633, Application US/0908975
Publication No. US2003016843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10633
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-10633

Query Match   1.2%; Score 60; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches   60; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db          1 CGTCCATGGTATCTACTGTAGTCCTGCAGATGGGAAATCCTATCCTACTAACAGCTGGCTC 60
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RESULT 2
US-10-431-627-3/c
Sequence 3, Application US/10431627
Publication No. US2004023885A1
; GENERAL INFORMATION:
; APPLICANT: Keen, Randy
; APPLICANT: Koder, Alan
; APPLICANT: Evans, David
; TITLE OF INVENTION: Apparatus for the Automated Synthesis of
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: 66663-031(EA5438)
; CURRENT APPLICATION NUMBER: US/10/431,627
; CURRENT FILING DATE: 2003-05-06

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c	549	16.8	0.3	21	1	US-10-786-720-12306	Sequence 12306, A
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c	608	16	0.3	20	1	US-10-714-796-233	Sequence 233, App
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c	673	15.4	0.3	18	1	US-10-333-429-322	Sequence 322, App
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c	679	15.4	0.3	20	1	US-10-309-362-98	Sequence 98, Appl
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c	683	15.4	0.3	20	1	US-10-481-613-156	Sequence 156, App
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c	685	15.4	0.3	20	1	US-11-011-500-98	Sequence 98, Appl
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c	687	15.2	0.3	20	1	US-10-160-786-98	Sequence 98, Appl
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OM nucleic - nucleic search, using sw model

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Run on: August 18, 2005, 08:50:58 ; Search time 45 seconds
3.758 Million cell updates/sec
(without alignments)

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Searched: 776 seqs, 16629 residues

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Post-processing: Minimum Match 0%
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Listing first 782 summaries

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SUMMARIES

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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; Patent No. 5648210
; GENERAL INFORMATION:
; APPLICANT: John W. Pierce

ALIGNMENTS

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Listing first 241 summaries

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and is derived by analysis of the total score distribution.

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80	16	0.3	20	1	US-09-065-058-1	Sequence 107, App
81	16	0.3	21	1	US-09-439-616-1	Sequence 1, Appli
82	16	0.3	21	1	US-08-486-047-8	Sequence 1, Appli
83	16	0.3	19	1	US-08-126-130-8	Sequence 8, Appli
84	15.8	0.3	19	1	US-09-467-023-167	Sequence 8, Appli
85	15.8	0.3	20	1	US-08-474-177-8	Sequence 167, App
86	15.8	0.3	20	1	US-09-422-978-4157	Sequence 8, Appli
87	15.8	0.3	20	1	US-08-487-033-8	Sequence 4157, Ap
88	15.8	0.3	20	1	US-08-480-010-8	Sequence 8, Appli
89	15.8	0.3	20	1	US-08-508-735-8	Sequence 8, Appli
90	15.8	0.3	20	1	US-08-848-251-8	Sequence 8, Appli
91	15.8	0.3	20	1	US-09-486-047-8	Sequence 8, Appli
92	15.8	0.3	20	1	US-09-120-130-8	Sequence 8, Appli
93	15.8	0.3	20	1	US-09-115-252-8	Sequence 8, Appli
94	15.8	0.3	20	1	US-08-986-515-8	Sequence 8, Appli
95	15.8	0.3	20	1	US-09-120-128-8	Sequence 167, App
96	15.8	0.3	20	1	US-09-120-129-8	Sequence 8, Appli
97	15.8	0.3	20	1	US-09-201-139-8	Sequence 8, Appli
98	15.8	0.3	20	1	US-09-120-131-8	Sequence 8, Appli
99	15.8	0.3	20	1	US-09-662-250A-36	Sequence 8, Appli
100	15.8	0.3	20	1	US-09-844-634-138	Sequence 36, Appl
101	15.8	0.3	20	1	US-09-322-409-143	Sequence 138, App
102	15.8	0.3	20	1	US-09-322-409-143	Sequence 143, App
103	15.8	0.3	20	1	US-09-451-527-143	Sequence 143, App
104	15.8	0.3	20	1	US-09-645-021-5	Sequence 5, Appli
105	15.8	0.3	20	1	US-09-456-090A-4	Sequence 4, Appli
106	15.8	0.3	20	1	US-09-227-800A-6	Sequence 6, Appli
106	15.8	0.3	20	1	US-08-921-954-6	Sequence 6, Appli

ID					Accession	Description
c 399	16.4	0.3	20	1	ABD221958	Human stanniocalci
c 400	16.4	0.3	20	1	ADK77211	Chimeric phosphoro
c 401	16.4	0.3	20	1	ADK76861	Chimeric phosphoro
c 402	16.4	0.3	20	1	ADK78504	Chimeric phosphoro
c 403	16.4	0.3	20	1	ADO71038	Human CD90 reverse
c 404	16.4	0.3	21	1	AAH62440	Proteasome 26S sub
c 405	16.4	0.3	21	1	AST08334	Human NOV4a PCR pr
c 406	16.4	0.3	21	1	ADH17700	Reverse PCR primer
c 407	16.2	0.3	21	1	AAQ86460	IFN-alpha nt723-73
c 408	16.2	0.3	21	1	AAC26585	Human Polymorphic
c 409	16.2	0.3	21	1	AAA475555	Primer for CTACK f
c 410	16.2	0.3	21	1	ABX11428	Human CTACK compet
c 411	16.2	0.3	21	1	ADB86772	rEST2 primer #2.
c 412	16.2	0.3	21	1	ADJ97635	Human Flt-1 DNA se
c 413	16.2	0.3	21	1	ADJ97636	Human Flt-1 DNA se
c 414	16	0.3	17	1	ADK00643	Human NOGO Hammerh
c 415	16	0.3	17	1	ADB40345	Tumour suppression
c 416	16	0.3	17	1	ADB45157	Tumour suppression
c 417	16	0.3	20	1	AAV37774	Analytical solid P
c 418	16	0.3	21	1	AAX89313	5'-phosphorylated
c 419	16	0.3	20	1	ABK50593	Streptomyces hygro
c 420	16	0.3	20	1	ADI35091	Human PLA2G1B gene
c 421	16	0.3	20	1	ADJ09992	PCR primer 8 to ge
c 422	16	0.3	20	1	ADP27118	Probe for CDK4I ge
c 423	16	0.3	21	1	ADR72469	Human matrix metal
c 424	16	0.3	21	1	AAZ93879	Antisense oligo ta
c 425	16	0.3	21	1	AAF95501	primer for amplify
c 426	15.8	0.3	19	1	AAZ22621	Human gene single
c 427	15.8	0.3	19	1	ADG35257	Adhalin gene fragm
c 428	15.8	0.3	19	1	ADG35995	Human biallelic ma
c 429	15.8	0.3	19	1	ADL79331	HIV siNA oligonucl
c 430	15.8	0.3	19	1	ADL79082	HIV siNA oligonucl
c 431	15.8	0.3	19	1	ADR77519	Human HER2 (BGFR2)
c 432	15.8	0.3	19	1	ADR80463	Human HER2 (BGFR2)
c 433	15.8	0.3	19	1	AAT15159	Human apolipoprote
c 434	15.8	0.3	19	1	AAQ99171	Probe for CDK4I ge
c 435	15.8	0.3	20	1	AAT169775	Human MTS1 exon2 P
c 436	15.8	0.3	20	1	AAV53825	Human multiple tum
c 437	15.8	0.3	20	1	AAV11244	Nucleotide sequenc
c 438	15.8	0.3	20	1	AAV70589	Seq IDH8 from US7
c 439	15.8	0.3	20	1	AAA95641	PCR primer 42F use
c 440	15.8	0.3	20	1	AAZ48780	Human MTS1 gene mu
c 441	15.8	0.3	20	1	AAZ39985	PCR primer for hum
c 442	15.8	0.3	19	1	AAA393359	PCR primer for hum
c 443	15.8	0.3	19	1	AAA393359	Human MTS related
c 444	15.8	0.3	20	1	AAA11171	Human MTS1 related
c 445	15.8	0.3	20	1	AAA11171	Human MTS1 gene ex
c 446	15.8	0.3	20	1	AA255597	Canine IL-13 sense
c 447	15.8	0.3	20	1	AAA90517	Oligonucleotide #8
c 448	15.8	0.3	20	1	AAH41615	Hco7 mice cDNA hea
c 449	15.8	0.3	20	1	AAF58177	Primer #7. Homo s
c 450	15.8	0.3	20	1	AAS02570	PCR primer #3 used
c 451	15.8	0.3	20	1	AAH29961	Mice of genotype H
c 452	15.8	0.3	20	1	AAD04699	Human multiple tum
c 453	15.8	0.3	20	1	AAH91454	Human inflammatory
c 454	15.8	0.3	20	1	AAC83077	Primer 42F for scr
c 455	15.8	0.3	20	1	AAL37733	Crygs gene related
c 456	15.8	0.3	20	1	AAL45671	Mammary gland bior
c 457	15.8	0.3	20	1	ABK68899	Mouse phosphorylas
c 458	15.8	0.3	20	1	ABO74888	Mouse TNFR2 antise
c 459	15.8	0.3	20	1	ADG24459	Heavy chain variab
c 460	15.8	0.3	20	1	ADG24508	Humanized antibody
c 461	15.8	0.3	20	1	ABX13334	Synthetic linker 8
c 462	15.8	0.3	20	1	ABX17785	Mouse urokinase pl
c 463	15.8	0.3	20	1	ABZ25516	Human MTS1 exon 2
c 464	15.8	0.3	20	1	ADB99900	Vitamin D nuclear
c 465	15.8	0.3	20	1	AAD64089	Human CDK4I' exon
c 466	15.8	0.3	20	1	ABF83451	Human CDK4I' exon
c 467	15.8	0.3	20	1	ABF87942	Human CDKN2A gene-
c 468	15.8	0.3	20	1	ABZ90375	Human oligonucleot
c 469	15.8	0.3	20	1	ABZ89500	Human oligonucleot
c 470	15.8	0.3	20	1	ABZ75637	Template (CTGA)5 f
c 471	15.8	0.3	20	1	ABD24172	Human calmodulin 2

ID					Accession	Description
c 472	15.8	0.3	20	1	ABD30273	AA284245-derived o
c 473	15.8	0.3	20	1	ABD25730	AA465687-derived o
c 474	15.8	0.3	20	1	ABD26605	AA909635-derived o
c 475	15.8	0.3	20	1	ABD64788	Human glucocortico
c 476	15.8	0.3	20	1	ADH64940	Human glucocortico
c 477	15.8	0.3	20	1	ADH54718	Human VEGF-C antis
c 478	15.8	0.3	20	1	ADH54788	Human VEGF-C antis
c 479	15.8	0.3	20	1	ADJ17090	Antisense DNA olig
c 480	15.8	0.3	20	1	ADJ16142	Antisense DNA olig
c 481	15.8	0.3	20	1	ADJ23137	Human endothelial
c 482	15.8	0.3	20	1	ADJ22653	Human endothelial
c 483	15.8	0.3	20	1	ADK81523	Chimeric phosphoro
c 484	15.8	0.3	20	1	ADK80970	Chimeric phosphoro
c 485	15.8	0.3	20	1	ADL59715	Human ESM-1 antise
c 486	15.8	0.3	20	1	ADL59601	Human ESM-1 antise
c 487	15.8	0.3	20	1	ADL59376	Human ESM-1 antise
c 488	15.8	0.3	20	1	ADL59258	Human ESM-1 antise
c 489	15.8	0.3	20	1	ADN35886	Osmolyte-stabilise
c 490	15.8	0.3	20	1	ADO53504	Farnesoid X recept
c 491	15.8	0.3	20	1	ADO53202	Farnesoid X recept
c 492	15.8	0.3	20	1	ADN01338	Endothelial differ
c 493	15.8	0.3	21	1	ADQ59323	KIAA1096 forward P
c 494	15.8	0.3	21	1	ADQ14094	CAPN3/DYSF PCR pri
c 495	15.8	0.3	21	1	AAV37276	5' PCR primer for
c 496	15.8	0.3	21	1	AAV27520	5' PCR primer for
c 497	15.8	0.3	21	1	AAZ74371	Banana EFE gene fr
c 498	15.8	0.3	21	1	ABA81997	Wound healing rela
c 499	15.8	0.3	21	1	ABA81999	Mouse wound healin
c 500	15.8	0.3	21	1	AAS09920	PCR primer #4 used
c 501	15.8	0.3	21	1	AAH62183	APLP2 polymorphism
c 502	15.8	0.3	21	1	ABK94358	Endothelin convert
c 503	15.8	0.3	21	1	ABK94357	Endothelin convert
c 504	15.8	0.3	21	1	ABV76147	Mouse alpha 1-anti
c 505	15.8	0.3	21	1	ACC58762	Pro-alpha1(II) col
c 506	15.8	0.3	21	1	ABZ75638	Template (CTGA) 5-A
c 507	15.8	0.3	21	1	ABK41074	Porcine PUUGE3 UP-
c 508	15.8	0.3	18	1	ABK00726	Procollagen I reve
c 509	15.4	0.3	17	1	ABZ77709	Human obesity-asso
c 510	15.4	0.3	17	1	ABK00962	PCR primer used to
c 511	15.4	0.3	17	1	ABK00963	PCR primer used to
c 512	15.4	0.3	17	1	ADR79520	Human apolipoprote
c 513	15.4	0.3	17	1	ADR76576	Human apolipoprote
c 514	15.4	0.3	20	1	AAO75326	Urease gene PCR pr
c 515	15.4	0.3	20	1	AAT45687	Helicobacter UreB
c 516	15.4	0.3	20	1	AAA13146	PI3K antisense inh
c 517	15.4	0.3	20	1	AAZ28930	Forward primer aa2
c 518	15.4	0.3	20	1	AAZ71844	Human biallelic ma
c 519	15.4	0.3	19	1	ABX03737	Human RECQL5 inhib
c 520	15.4	0.3	18	1	ADR05333	Silkworm juvenile
c 521	15.4	0.3	17	1	ABD42797	Tumour suppression
c 522	15.4	0.3	17	1	ABB39787	Tumour suppression
c 523	15.4	0.3	20	1	ACC65135	Murine oligonucleo
c 524	15.4	0.3	20	1	ACC68083	Murine oligonucleo
c 525	15.4	0.3	20	1	ABK00963	Human NOGO Inozyme
c 526	15.4	0.3	20	1	ABK00963	Human NOGO Inozyme
c 527	15.4	0.3	20	1	AG70287	CLLD8 exon 12 and
c 528	15.4	0.3	20	1	ACC82889	CLLD8 exon 12 and
c 529	15.4	0.3	20	1	ADH66356	Human TRIP6 antise
c 530	15.4	0.3	20	1	ADH66905	Mouse TNFR2 antise
c 531	15.4	0.3	20	1	ADJ23055	Human endothelial
c 532	15.4	0.3	20	1	ADJ22915	Human endothelial
c 533	15.4	0.3	20	1	ADK81043	Human glucocortico
c 534	15.4	0.3	20	1	ADK76762	Human glucocortico
c 535	15.4	0.3	20	1	ADN12104	Chimeric phosphoro
c 536	15.4	0.3	20	1	ADO54095	Chimeric phosphoro
c 537	15.4	0.3	20	1	ADO53680	Primer of the inve
c 538	15.4	0.3	20	1	ADT01052	Farnesoid X recept
c 539	15.2	0.3	20	1	ADH26724	Farnesoid X recept
c 540	15.2	0.3	20	1	ADH26792	Human PI3K regulat
c 541	15.2	0.3	20	1	ADL34613	Human PI3K regulat
c 542	15.2	0.3	20	1	ADL34681	Phosphoinositide-3

ID					Accession	Description
c 253	20	0.4	20	1	ADL34628	ISIS antisense oli
c 254	20	0.4	20	1	ADL34635	ISIS antisense oli
c 255	20	0.4	20	1	ADL34650	Phosphoinositide-3
c 256	20	0.4	20	1	ADL34667	Phosphoinositide-3
c 257	20	0.4	20	1	ADL34573	ISIS antisense oli
c 258	20	0.4	20	1	ADL34581	ISIS antisense oli
c 259	20	0.4	20	1	ADL34612	ISIS antisense oli
c 260	20	0.4	20	1	ADL34644	Phosphoinositide-3
c 261	20	0.4	20	1	ADL34658	Phosphoinositide-3
c 262	20	0.4	20	1	ADL34674	Phosphoinositide-3
c 263	20	0.4	20	1	ADL34568	Phosphoinositide-3
c 264	20	0.4	20	1	ADL34569	Phosphoinositide-3
c 265	20	0.4	20	1	ADL34570	ISIS antisense oli
c 266	20	0.4	20	1	ADL34615	ISIS antisense oli
c 267	20	0.4	20	1	ADL34619	ISIS antisense oli
c 268	20	0.4	20	1	ADL34582	Phosphoinositide-3
c 269	20	0.4	20	1	ADL34587	Phosphoinositide-3
c 270	20	0.4	20	1	ADL34609	ISIS antisense oli
c 271	20	0.4	20	1	ADL34579	Phosphoinositide-3
c 272	20	0.4	20	1	ADL34641	ISIS antisense oli
c 273	20	0.4	20	1	ADL34648	Phosphoinositide-3
c 274	20	0.4	20	1	ADL34673	Phosphoinositide-3
c 275	20	0.4	20	1	ADL34685	Phosphoinositide-3
c 276	20	0.4	20	1	ADL34557	ISIS antisense oli
c 277	20	0.4	20	1	ADL34574	ISIS antisense oli
c 278	20	0.4	20	1	ADL34584	ISIS antisense oli
c 279	20	0.4	20	1	ADL34632	ISIS antisense oli
c 280	20	0.4	20	1	ADL34672	Phosphoinositide-3
c 281	20	0.4	20	1	ADL34679	Phosphoinositide-3
c 282	20	0.4	20	1	ADL34688	Phosphoinositide-3
c 283	20	0.4	20	1	ADL34696	Phosphoinositide-3
c 284	20	0.4	20	1	ADL34701	ISIS antisense oli
c 285	20	0.4	20	1	ADL34572	ISIS antisense oli
c 286	20	0.4	20	1	ADL34575	ISIS antisense oli
c 287	20	0.4	20	1	ADL34578	ISIS antisense oli
c 288	20	0.4	20	1	ADL34604	ISIS antisense oli
c 289	20	0.4	20	1	ADL34634	ISIS antisense oli
c 290	20	0.4	20	1	ADL34653	Phosphoinositide-3
c 291	20	0.4	20	1	ADL34670	Phosphoinositide-3
c 292	20	0.4	20	1	ADL34678	Phosphoinositide-3
c 293	20	0.4	20	1	ADL34698	Phosphoinositide-3
c 294	20	0.4	20	1	ADL34565	ISIS antisense oli
c 295	20	0.4	20	1	ADL34575	ISIS antisense oli
c 296	20	0.4	20	1	ADL34604	ISIS antisense oli
c 297	20	0.4	20	1	ADL34642	ISIS antisense oli
c 298	20	0.4	20	1	ADL34645	Phosphoinositide-3
c 299	20	0.4	20	1	ADL34668	Phosphoinositide-3
c 300	20	0.4	20	1	ADL34676	Phosphoinositide-3
c 301	20	0.4	20	1	ADL34690	Phosphoinositide-3
c 302	20	0.4	20	1	ADL34692	Phosphoinositide-3
c 303	20	0.4	20	1	ADL34566	ISIS antisense oli
c 304	20	0.4	20	1	ADL34631	ISIS antisense oli
c 305	20	0.4	20	1	ADL34655	ISIS antisense oli
c 306	20	0.4	20	1	ADL34661	Phosphoinositide-3
c 307	20	0.4	20	1	ADL34665	Phosphoinositide-3
c 308	20	0.4	20	1	ADL34683	Phosphoinositide-3
c 309	20	0.4	21	1	ADR69805	Phosphoinositide-3
c 310	20	0.4	21	1	AAX08666	Primer used for su
c 311	20	0.4	21	1	AAF73394	Micro-channel mole
c 312	20	0.4	24	1	ADK65560	A gossypii ribofla
c 313	19.6	0.4	24	1	AAQ47178	Grand fir monoterp
c 314	19.6	0.4	26	1	ABA01951	Human hantavirus
c 315	19.4	0.4	24	1	AAP98935	Hantaan hantavirus
c 316	19.2	0.4	24	1	ABS77576	MHC DR A intron bi
c 317	19.2	0.4	24	1	ACD99368	Human TNF receptor
c 318	19.2	0.4	24	1	ADG76537	Immunostimulatory
c 319	19.2	0.4	24	1	ADG76001	Immunostimulatory
c 320	19.2	0.4	24	1	ADG76035	Angiogenesis inhib
c 321	19.2	0.4	24	1	ACI76263	Immunostimulatory
c 322	19.2	0.4	25	1	ACI76262	Non-CpG DNA oligon
c 323	19.2	0.4	25	1	ADO57809	Non-CpG DNA oligon
c 324	19	0.4	19	1	ADR82260	Human microarray D
c 325	19	0.4	19	1		Hepatitis C virus

ID					Accession	Description
c 326	19	0.4	19	1	ADR82257	Hepatitis C virus
c 327	19	0.4	19	1	ADR82261	Hepatitis C virus
c 328	19	0.4	19	1	ADR82258	Hepatitis C virus
c 329	19	0.4	19	1	ADR82256	Hepatitis C virus
c 330	19	0.4	20	1	ADR82259	Hepatitis C virus
c 331	18.4	0.4	20	1	AAT32292	Primer for manipul
c 332	18.4	0.4	20	1	ACF79629	Thiopurine S-methy
c 333	18.4	0.4	22	1	AAH75578	Human transcriptio
c 334	18.4	0.4	24	1	ADR36253	Rhodosporidium mut
c 335	18.2	0.4	24	1	ABQ07017	Murine alpha-l-idu
c 336	18.2	0.4	24	1	ABO78896	Human zinc finger
c 337	18.2	0.4	24	1	AAS19218	Kringle protein 14
c 338	18.2	0.4	24	1	ABS59876	Human protease reg
c 339	18.2	0.4	24	1	ADO81152	Prion protein poly
c 340	18	0.4	18	1	ADR32355	Rat KDR cytosolic
c 341	18	0.4	18	1	ADR57967	Nucleotide #4 for
c 342	18	0.4	22	1	AAA63751	Primer #24 in inve
c 343	17.8	0.4	21	1	ABA10153	2'-MOE gapmer anti
c 344	17.8	0.4	22	1	ABR32218	Antisense 2'-MOE g
c 345	17.4	0.4	24	1	AAT87932	Molecular beacon h
c 346	17.4	0.4	18	1	AAQ92371	Acetylated aminopr
c 347	17.4	0.4	19	1	AAH45480	DNA primer. Synth
c 348	17.4	0.4	19	1	AAB83687	PCR primer specifi
c 349	17.4	0.4	20	1	AAH58849	cdk-we-hu ribozyme
c 350	17.4	0.4	20	1	AAS14499	cdk-we-hu ribozyme
c 351	17.4	0.4	22	1	ADH18861	Human Vbeta gene r
c 352	17.4	0.4	22	1	AAQ23402	4 synthesis-period
c 353	17.4	0.4	23	1	ABL57072	2'-MOE gapmer anti
c 354	17.4	0.4	22	1	ADR42646	Antisense 2'-MOE g
c 355	17.2	0.3	22	1	ADH70614	Human Vbeta gene r
c 356	17.2	0.3	22	1	ADO10062	4 synthesis-period
c 357	17.2	0.3	22	1	ADR32106	Hepatitis B virus
c 358	17.2	0.3	22	1	ADR67796	Hepatitis B virus
c 359	17	0.3	17	1	AAT66995	Hepatitis B virus
c 360	17	0.3	17	1	AAT90091	Primer for amplify
c 361	17	0.3	17	1	AAT69930	Vector-specific pr
c 362	17	0.3	22	1	AAH12632	Primer SK-Zap for
c 363	17	0.3	17	1	ADJ45219	T3 PCR primer for
c 364	17	0.3	20	1	AAD15659	PCR primer used to
c 365	17	0.3	17	1	AAH25194	Mch6 cloning prime
c 366	17	0.3	20	1	ADE52023	Primer for DNA enc
c 367	17	0.3	20	1	ADR81681	Mammalian ced-3 ho
c 368	17	0.3	22	1	AAT18426	1,5-anhydroglucito
c 369	16.8	0.3	20	1	AAH20641	Human JAGGED1 gene
c 370	16.8	0.3	20	1	ADK80790	Negative control P
c 371	16.8	0.3	20	1	ADL59618	Human ESM-1 antise
c 372	16.8	0.3	20	1	ADL59444	VLDLr gene, single
c 373	16.8	0.3	20	1	ADL59682	Human endothelial
c 374	16.8	0.3	21	1	AAS11777	Human ESM-1 antise
c 375	16.8	0.3	20	1	ACC57852	Chimeric phosphoro
c 376	16.8	0.3	20	1	ADM94102	Human ESM-1 antise
c 377	16.8	0.3	20	1	ADQ90421	Human ESM-1 antise
c 378	16.8	0.3	20	1	AAV27859	TCRB tubes A and B
c 379	16.8	0.3	21	1	AAX80013	PCR primer H used
c 380	16.8	0.3	21	1	AAA01162	Mouse VEGF reverse
c 381	16.8	0.3	21	1	AAD44228	PCR primer H used
c 382	16.8	0.3	22	1	ABS70799	B. thuringiensis c
c 383	16.8	0.3	22	1	ABS59856	B. thuringiensis c
c 384	16.8	0.3	22	1	AAD64016	B. thuringiensis c
c 385	16.8	0.3	22	1	ACF42669	PCR primer H used
c 386	16.8	0.3	22	1	ADI04018	B. thuringiensis c
c 387	16.8	0.3	22	1	ADO16768	PCR primer H used
c 388	16.8	0.3	22	1	ADM06310	PCR primer H used
c 389	16.8	0.3	22	1	ACI04018	Human ALMS1 PCR pr
c 390	16.8	0.3	22	1	ADO16768	Bovine GHR exon am
c 391	16.8	0.3	22	1	ACF42669	4 synthesis-period
c 392	16.8	0.3	22	1	AAD64016	Human PCR primer S
c 393	16.4	0.3	22	1	ADI04018	Human PCR primer S
c 394	16.4	0.3	18	1	ADM06310	S. aureus coding B
c 395	16.4	0.3	19	1	AAX33800	PCR primer for clo
c 396	16.4	0.3	22	1	AAX76854	Human TNFR2 antise
c 397	16.4	0.3	20	1	ABQ74807	Human oligonucleot
c 398	16.4	0.3	20	1	ABZ85728	Hepatitis C virus

c	107	20	0.4	20	1	ADH26758 Human PI3K regulat
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	182	20	0.4	20	1	ADJ34677 Phosphoinositide-3
	183	20	0.4	20	1	ADJ34700 Phosphoinositide-3
	184	20	0.4	20	1	ADJ34602 Phosphoinositide-3
c	185	20	0.4	20	1	ADJ34605 ISIS antisense oli
	186	20	0.4	20	1	ADJ34651 Phosphoinositide-3
	187	20	0.4	20	1	ADJ34671 Phosphoinositide-3
	188	20	0.4	20	1	ADJ34699 Phosphoinositide-3
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	205	20	0.4	20	1	ADJ34682 Phosphoinositide-3
	206	20	0.4	20	1	ADJ34684 Phosphoinositide-3
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c	252	20	0.4	20	1	ADJ34627 ISIS antisense oli

OM nucleic - nucleic search, using sw model

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Run on: August 18, 2005, 08:36:54 ; Search time 32 Seconds (without alignments)
3.559 Million cell updates/sec

Title: US-10-667-022-4
Perfect score: 5085
Sequence: 1 ggatcccccgggctgcagga..........tcgaggggggcccggtacc 5085
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5
Searched: 536 seqs, 11197 residues
Total number of hits satisfying chosen parameters: 1072
Minimum Match 0%
Maximum Match 100%
Maximum DB seq length: 80
Minimum DB seq length: 8
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 542 summaries
Database :   fetching.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	60	1.2	60	1	ABN37885	Human spliced tran
c	2	44	0.9	54	1	ACN54858	Cotton androecium
c	3	41.2	0.8	51	1	ACN52123	Cotton androecium
c	4	41.2	0.8	51	1	ACN51219	Cotton androecium
c	5	40.6	0.8	50	1	ADS74280	T50 element used i
c	6	40.6	0.8	50	1	ADS74279	A50 element used i
c	7	37.8	0.7	50	1	ADR18577	Oligonucleotide oc
c	8	33.8	0.7	43	1	ADI97735	238P1B2 gene relat
c	9	33.2	0.7	40	1	AAQ36506	Sequence of the 5'
c	10	27.6	0.7	40	1	AAT93816	Antitumoural phosp
c	11	27	0.5	35	1	AAT93815	Antitumoural phosp
c	12	27	0.5	35	1	AAT93823	Antitumoural phosp
c	13	26	0.5	35	1	ADH26672	Human phosphoinosi
c	14	26	0.5	26	1	ADL34561	Human phosphoinosi
c	15	26	0.5	34	1	AAC90605	Tomato spotted wil
c	16	25.4	0.5	27	1	ADR51048	Duo binding moiety
c	17	24	0.5	24	1	ADR48246	Microarray synthes
c	18	24	0.5	24	1	ADR48249	Microarray synthes
c	19	24	0.5	30	1	AAT68809	Levansucrase mutan
c	20	23	0.5	23	1	ADH26671	Human PI3K regulat
c	21	23	0.5	23	1	ADH26670	Human PI3K regulat
c	22	23	0.5	23	1	ADL34559	Human phosphoinosi
c	23	23	0.5	25	1	ADL34560	Human phosphoinosi
c	24	22	0.4	21	1	ADR44220	Caenorhabditis ele
c	25	21	0.4	24	1	AAV03154	PCR primer BKSBE u
c	26	21	0.4	24	1	AAV60992	Inverse PCR primer
c	27	21	0.4	24	1	ABA02435	Human GM2 activati
c	28	21	0.4	24	1	ABA95961	Human molecular ch
c	29	21	0.4	24	1	ABZ57354	Human zinc finger
c	30	21	0.4	24	1	ADR44221	Caenorhabditis ele
c	31	20.4	0.4	24	1	ABA95469	Human natural kill
c	32	20.2	0.4	22	1	ADS13095	Oligo dT PCR prime
c	33	20	0.4	20	1	AAF76082	pBluescript vector
c	34	20	0.4	20	1	AAF76469	Maize ZmMADS2 codi
c	35	20	0.4	20	1	ADH26676	Human PI3K regulat
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c 113	15.8	0.3	20	1	AR241587	ACCESSION:AR241587
c 114	15.8	0.3	20	1	AR254543	ACCESSION:AR254543
c 115	15.8	0.3	20	1	AR352007	ACCESSION:AR352007
c 116	15.8	0.3	20	1	AR454044	ACCESSION:AR454044
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c 126	15.8	0.3	21	1	AX754893	ACCESSION:AX754893
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c 128	15.8	0.3	21	1	BD079124	ACCESSION:BD079124
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c 130	15.4	0.3	17	1	AX215520	ACCESSION:AX215520
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c 132	15.4	0.3	17	1	AX724695	ACCESSION:AX724695
c 133	15.4	0.3	17	1	AX727643	ACCESSION:AX727643
c 134	15.4	0.3	17	1	AX756789	ACCESSION:AX756789
c 135	15.4	0.3	18	1	AX759799	ACCESSION:AX759799
c 136	15.4	0.3	18	1	AX378533	ACCESSION:AX378533
c 137	15.4	0.3	18	1	AX765627	ACCESSION:AX765627
c 138	15.4	0.3	18	1	BD124158	ACCESSION:BD124158
c 139	15.4	0.3	20	1	A73298	ACCESSION:A73298
c 140	15.4	0.3	20	1	AR061035	ACCESSION:AR061035
c 141	15.4	0.3	20	1	AR161668	ACCESSION:AR161668
c 142	15.4	0.3	20	1	BD228503	ACCESSION:BD228503
c 143	15.4	0.3	20	1	AR231312	ACCESSION:AR231312
c 144	15.4	0.3	20	1	AR294465	ACCESSION:AR294465
c 145	15.4	0.3	20	1	AR308288	ACCESSION:AR308288
c 146	15.4	0.3	20	1	AR359728	ACCESSION:AR359728
c 147	15.4	0.3	20	1	AX010862	ACCESSION:AX010862
c 148	15.4	0.3	20	1	AX029045	ACCESSION:AX029045
c 149	15.4	0.3	20	1	AX699215	ACCESSION:AX699215
c 150	15.4	0.3	20	1	BD009330	ACCESSION:BD009330

ALIGNMENTS

RESULT 1
LOCUS   CQ540998
DEFINITION Sequence 10633 from Patent WO0210449.
ACCESSION   CQ540998
VERSION   CQ540998.1 GI:41507262
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE   Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
JOURNAL   Patent: WO 0210449-A 10633 07-FEB-2002;
            Compugen Inc. (US)
FEATURES   Location/Qualifiers
     source   1..60
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

            CQ540998 60 bp   DNA   linear   PAT   30-JAN-2004

Best Local Similarity   100.0%; Pred. No. 0.0069;
Matches   60; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4290 CGTCCATGGTATCTACTTGTAGTCCTGCCAGATGGAAATCCTATCCTACTAACAGCTGGCTC 4349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGTCCATGGTATCTACTTGTAGTCCTGCCAGATGGAAATCCTATCCTACTAACAGCTGGCTC   60

Query Match 91.2%; Score 60; DB 1; Length 60;

RESULT 2
LOCUS   CQ878333
DEFINITION Sequence 35 from Patent WO2004081179.
ACCESSION   CQ878333
VERSION   CQ878333.1 GI:53790899
KEYWORDS
SOURCE   synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS   Lai,W.S. and Blackshear,P.J.
TITLE   Regulation of rna stability
JOURNAL   Patent: WO 2004081179-A 35 23-SEP-2004;
            The Government of the United States of America (US)
FEATURES   Location/Qualifiers
     source   1..50
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Synthetic
                     nucleotide sequence"

            CQ878333 Sequence 35 from Patent WO2004081179.   50 bp   DNA   linear   PAT   04-OCT-2004

Query Match 0.8%; Score 40.6; DB 1; Length 50;
Best Local Similarity   91.5%; Pred. No. 0.51;
Matches   43; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   5018 AAACTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5064
           ||| |||||||||||||||||||||||||||||||||||||||||||
Db   1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   47

RESULT 3
CQ878334/c
LOCUS   CQ878334
DEFINITION Sequence 36 from Patent WO2004081179.
ACCESSION   CQ878334
VERSION   CQ878334.1 GI:53790900
            CQ878334 Sequence 36 from Patent WO2004081179.   50 bp   DNA   linear   PAT   04-OCT-2004
KEYWORDS
SOURCE   synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS   Lai,W.S. and Blackshear,P.J.
TITLE   Regulation of rna stability
JOURNAL   Patent: WO 2004081179-A 36 23-SEP-2004;
            The Government of the United States of America (US)
FEATURES   Location/Qualifiers
     source   1..50
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Synthetic
                     nucleotide sequence"

Query Match 0.8%; Score 40.6; DB 1; Length 50;
Best Local Similarity   91.5%; Pred. No. 0.51;
Matches   43; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   5018 AAACTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5064
           ||| |||||||||||||||||||||||||||||||||||||||||||
Db   50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   4

RESULT 4

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: August 18, 2005, 08:32:01 ; Search time 9 Seconds
(without alignments)
3.614 Million cell updates/sec

Title: US-10-667-022-4
Perfect score: 5085
Sequence: 1 ggatccccgggctgcagga..................tcgagggggggccggtacc 5085

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 150 seqs, 3198 residues

Total number of hits satisfying chosen parameters: 300

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : fetch4rge.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	60	1.2	60	1	CQ540998	ACCESSION:CQ540998
2	40.6	0.8	50	1	CQ878333	ACCESSION:CQ878333
3	40.6	0.8	50	1	CQ878334	ACCESSION:CQ878334
4	33.2	0.7	40	1	AR014711	ACCESSION:AR014711
5	33.2	0.7	40	1	I55635	ACCESSION:I55635
6	30	0.6	30	1	AR541545	ACCESSION:AR541545
7	30	0.6	30	1	AR541546	ACCESSION:AR541546
8	27.6	0.5	35	1	A63566	ACCESSION:A63566
9	27	0.5	35	1	A63565	ACCESSION:A63565
10	27	0.5	35	1	A63574	ACCESSION:A63574
11	22.6	0.4	30	1	AR559409	ACCESSION:AR559409
12	21	0.4	21	1	E13974	ACCESSION:E13974
13	21	0.4	21	1	E14908	ACCESSION:E14908
14	21	0.4	21	1	E64706	ACCESSION:E64706
15	21	0.4	24	1	AR559758	ACCESSION:AR559758
16	21	0.4	24	1	A87299	ACCESSION:A87299
17	21	0.4	20	1	BD057377	ACCESSION:BD057377
18	20	0.4	20	1	AR532682	ACCESSION:AR532682
19	20	0.4	20	1	AR559396	ACCESSION:AR559396
20	20	0.4	20	1	AR559411	ACCESSION:AR559411
21	20	0.4	20	1	AR561993	ACCESSION:AR561993
22	20	0.4	20	1	AX565165	ACCESSION:AX565165
23	20	0.4	20	1	AX085373	ACCESSION:AX085373
24	20	0.4	20	1	AX085176	ACCESSION:AX085176
25	20	0.4	21	1	CQ855140	ACCESSION:CQ855140
26	20	0.4	24	1	AR222119	ACCESSION:AR222119
27	19.2	0.4	24	1	AX546921	ACCESSION:AX546921
28	19.2	0.4	24	1	AX103868	ACCESSION:AX103868
29	19	0.4	19	1	CQ817044	ACCESSION:CQ817044
30	19	0.4	19	1	AR541350	ACCESSION:AR541350
31	19	0.4	19	1	AR541351	ACCESSION:AR541351
32	19	0.4	19	1	AR541352	ACCESSION:AR541352
33	19	0.4	19	1	AR541353	ACCESSION:AR541353
34	19	0.4	19	1	AR541361	ACCESSION:AR541361
35	19	0.4	20	1	AR562157	ACCESSION:AR562157
36	18.8	0.4	25	1	AR239256	ACCESSION:AR239256
37	18.8	0.4	25	1	AX279058	ACCESSION:AX279058
38	18.4	0.4	20	1	A52122	ACCESSION:A52122
39	18.4	0.4	20	1	AR068314	ACCESSION:AR068314
40	18.4	0.4	22	1	AX815621	ACCESSION:AX815621
41	18.4	0.4	22	1	AX815622	ACCESSION:AX815622
42	18.2	0.4	19	1	AR528447	ACCESSION:AR528447
43	18	0.4	19	1	SSA7777	ACCESSION:AJ000777
44	18	0.4	20	1	AR720061	ACCESSION:AR720061
45	18	0.4	19	1	AR562158	ACCESSION:AR562158
46	18	0.4	20	1	AR562156	ACCESSION:AR562156
47	17.4	0.3	19	1	AX130055	ACCESSION:AX130055
48	17.4	0.3	21	1	AX498248	ACCESSION:AX498248
49	17.4	0.3	17	1	AR067856	ACCESSION:AR067856
50	17	0.3	17	1	AR164207	ACCESSION:AR164207
51	17	0.3	17	1	AR164645	ACCESSION:AR164645
52	17	0.3	17	1	AR168088	ACCESSION:AR168088
53	17	0.3	17	1	AR232188	ACCESSION:AR232188
54	17	0.3	21	1	AR256040	ACCESSION:AR256040
55	17	0.3	17	1	AR337628	ACCESSION:AR337628
56	17	0.3	17	1	AR473351	ACCESSION:AR473351
57	17	0.3	17	1	AR492475	ACCESSION:AR492475
58	17	0.3	17	1	AR533532	ACCESSION:AR533532
59	17	0.3	20	1	AR024174	ACCESSION:AR024174
60	17	0.3	20	1	AR060565	ACCESSION:AR060565
61	17	0.3	20	1	I54907	ACCESSION:I54907
62	17	0.3	20	1	AR370189	ACCESSION:AR370189
63	16.8	0.3	20	1	AR136554	ACCESSION:AR136554
64	16.8	0.3	18	1	E60050	ACCESSION:E60050
65	16.8	0.3	19	1	AR179243	ACCESSION:AR179243
66	16.8	0.3	20	1	BD078905	ACCESSION:BD078905
67	16.8	0.3	22	1	A95627	ACCESSION:A95627
68	16.8	0.3	20	1	AR215742	ACCESSION:AR215742
69	16.8	0.3	22	1	AR429226	ACCESSION:AR429226
70	16.8	0.3	22	1	BD091431	ACCESSION:BD091431
71	16.8	0.3	21	1	AX247921	ACCESSION:AX247921
72	16.8	0.3	22	1	AX675429	ACCESSION:AX675429
73	16.8	0.3	21	1	CQ881300	ACCESSION:CQ881300
74	16.4	0.3	21	1	AX937073	ACCESSION:AX937073
75	16.4	0.3	20	1	CQ801070	ACCESSION:CQ801070
76	16.4	0.3	22	1	AR120179	ACCESSION:AR120179
77	16.4	0.3	20	1	AR126177	ACCESSION:AR126177
78	16.4	0.3	22	1	AR177993	ACCESSION:AR177993
79	16.4	0.3	22	1	AR220297	ACCESSION:AR220297
80	16.4	0.3	21	1	AX751620	ACCESSION:AX751620
81	16.4	0.3	21	1	BD063767	ACCESSION:BD063767
82	16.2	0.3	21	1	AX837871	ACCESSION:AX837871
83	16.2	0.3	21	1	AR482351	ACCESSION:AR482351
84	16.2	0.3	20	1	AR165554	ACCESSION:AR165554
85	16	0.3	21	1	AR561628	ACCESSION:AR561628
86	16	0.3	16	1	AR561693	ACCESSION:AR561693
87	16	0.3	16	1	AX951931	ACCESSION:AX951931
88	16	0.3	16	1	AX215201	ACCESSION:AX215201
89	16	0.3	20	1	AX757347	ACCESSION:AX757347
90	16	0.3	16	1	AX762159	ACCESSION:AX762159
91	16	0.3	16	1	AR148114	ACCESSION:AR148114
92	16	0.3	16	1	AR173949	ACCESSION:AR173949
93	16	0.3	16	1	AR173955	ACCESSION:AR173955
94	16	0.3	16	1	BD271297	ACCESSION:BD271297
95	16	0.3	21	1	BD271303	ACCESSION:BD271303
96	15.8	0.3	21	1	AX154243	ACCESSION:AX154243
97	15.8	0.3	19	1	I95654	ACCESSION:I95654
98	15.8	0.3	19	1	AR292422	ACCESSION:AR292422
99	15.8	0.3	20	1	AR001320	ACCESSION:AR001320
100	15.8	0.3	20	1	AR037500	ACCESSION:AR037500
101	15.8	0.3	20	1	AR062780	ACCESSION:AR062780
102	15.8	0.3	20	1	AR087858	ACCESSION:AR087858
103	15.8	0.3	20	1	AR091328	ACCESSION:AR091328
104	15.8	0.3	20	1	AR118034	ACCESSION:AR118034
105	15.8	0.3	20	1	AR127753	ACCESSION:AR127753
106	15.8	0.3	20	1	AR144920	ACCESSION:AR144920

OM nucleic - nucleic search, using sw model

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Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 18, 2005, 09:13:44 ; Search time 5 Seconds
                (without alignments)
                3.936 Million cell updates/sec

Title: US-10-667-022-4
Perfect score: 5085
Sequence: 1 ggatcccccgggctgcagga..........tcgagggggggcccggtacc 5085

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5
Searched: 58 seqs, 1935 residues
Total number of hits satisfying chosen parameters: 116
Minimum DB seq length: 8
Maximum DB seq length: 80
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 58 summaries

Database :   fetch4rst.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	C	Score	% Query Match	Match Length	DB	ID	Description
1		44.4	0.9	56	1	CV058129	ACCESSION:CV058129
2		42	0.8	53	1	CV065817	ACCESSION:CV065817
3		41.4	0.8	45	1	CV066098	ACCESSION:CV066098
4		41.4	0.8	46	1	CV059173	ACCESSION:CV059173
5		41.4	0.8	48	1	CV064988	ACCESSION:CV064988
6		41	0.8	54	1	CV057724	ACCESSION:CV057724
7		41	0.8	54	1	CV307126	ACCESSION:CV307126
8		40.4	0.8	46	1	CV061744	ACCESSION:CV061744
9		39.6	0.8	54	1	CV063340	ACCESSION:CV063340
10	c	39.6	0.8	51	1	CW509332	ACCESSION:CW509332
11	c	39.4	0.8	43	1	CV062138	ACCESSION:CV062138
12		38.4	0.8	42	1	CV062024	ACCESSION:CV062024
13	c	36.6	0.7	47	1	CV060361	ACCESSION:CV060361
14	c	36.6	0.7	47	1	CV060559	ACCESSION:CV060559
15	c	35.6	0.7	44	1	CV060847	ACCESSION:CV060847
16	c	35.6	0.7	47	1	CV061673	ACCESSION:CV061673
17	c	35.6	0.7	47	1	CV06153	ACCESSION:CV06153
18		34.8	0.7	47	1	CV055836	ACCESSION:CV055836
19		34.4	0.7	38	1	CV064759	ACCESSION:CV064759
20		34.4	0.7	40	1	CR762707	ACCESSION:CR762707
21	c	33.6	0.7	40	1	CW509301	ACCESSION:CW509301
22	c	33.6	0.7	40	1	CV064457	ACCESSION:CV064457
23		32.8	0.6	41	1	CV054826	ACCESSION:CV054826
24	c	32.4	0.6	36	1	CV066718	ACCESSION:CV066718
25	c	31.4	0.6	35	1	CV066327	ACCESSION:CV066327
26	c	30.4	0.6	36	1	CV091545	ACCESSION:CV091545
27	c	30.4	0.6	37	1	CV052204	ACCESSION:CV052204
28	c	30	0.6	36	1	CW020481	ACCESSION:CW020481
29	c	29.8	0.6	30	1	CV064432	ACCESSION:CV064432
30	c	29.4	0.6	35	1	CV020481	ACCESSION:CV020481
31	c	27	0.5	31	1	CV057897	ACCESSION:CV057897
32	c	25	0.5	28	1	CF305592	ACCESSION:CF305592
33		24.8	0.5	33	1	R38731	ACCESSION:R38731
34		24.6	0.5	31	1	CV066570	ACCESSION:CV066570
34		24.6	0.5	31	1	AI153615	ACCESSION:AI153615
35	c	24.4	0.5	31	1	BW588370	ACCESSION:BW588370
36	c	22.8	0.4	26	1	CW020478	ACCESSION:CW020478
37	c	22.8	0.4	28	1	CV091538	ACCESSION:CV091538
38		21.4	0.4	28	1	CV065010	ACCESSION:CV065010
39		20	0.4	20	1	CF305590	ACCESSION:CF305590
40		19.4	0.4	20	1	CV064628	ACCESSION:CV064628
41		19.4	0.4	23	1	CV066488	ACCESSION:CV066488
42	c	19.2	0.4	24	1	AZ308225	ACCESSION:AZ308225
43	c	19.2	0.4	24	1	AZ814559	ACCESSION:AZ814559
44	c	19.2	0.4	24	1	AL483684	ACCESSION:AL483684
45	c	18.8	0.4	24	1	TA250E05P	ACCESSION:TA250E05P
46	c	18	0.4	19	1	AZ827015	ACCESSION:AZ827015
47	c	17.8	0.4	21	1	AZ597932	ACCESSION:AZ597932
48		17	0.3	19	1	CF303019	ACCESSION:CF303019
49		17	0.3	19	1	CO578459	ACCESSION:CO578459
50		16.4	0.3	18	1	AJ725584	ACCESSION:AJ725584
51	c	16.4	0.3	18	1	CR786637	ACCESSION:CR786637
52	c	16	0.3	16	1	AJ679356	ACCESSION:AJ679356
53		16	0.3	16	1	CR786853	ACCESSION:CR786853
54		16	0.3	17	1	BM398023	ACCESSION:BM398023
55		16	0.3	17	1	BM398024	ACCESSION:BM398024
56		16	0.3	17	1	BM399768	ACCESSION:BM399768
57		16	0.3	20	1	CF307519	ACCESSION:CF307519
58		16	0.3	20	1	CF326591	ACCESSION:CF326591

ALIGNMENTS

RESULT 1
CV058129/c

```
LOCUS       CV058129      56 bp    mRNA    linear    EST  24-AUG-2004
DEFINITION  BNBL34f4 Barley EST endosperm library Hordeum vulgare subsp.
            vulgare cDNA clone BNBL34f4 5' similar to Unknown Function, mRNA
            sequence.
ACCESSION   CV058129
VERSION     CV058129.1  GI:51521268
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Ali,S.,Holloway,B. and Taylor,W.C.
  TITLE     Normalisation of cereal endosperm EST libraries for structural and
            functional genomic analysis
  JOURNAL   Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT     Contact: Bill Taylor
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
            Seq primer: M13 reverse primer
            High quality sequence stop: 56.
FEATURES             Location/Qualifiers
     source          1..56
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Himalaya"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="BNBL34f4"
                     /tissue_type="endosperm"
                     /dev_stage="developing endosperm tissue 10, 12, 15 dpa
                     (days post anthesis)"
                     /lab_host="DH10B (Life Technology)"
                     /clone_lib="Barley EST endosperm library"
                     /note="vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
                     was prepared from endosperm tissues of the Barley cultivar
```

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.